Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

1-41 (Cancelled).

42. (Withdrawn) An aptamer that specifically binds to a target, the target being capable of binding to a target partner, wherein the binding of the aptamer to the target regulates the binding of the target to the target partner.

43. (Withdrawn) The aptamer of claim 42, wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner.

44. (Withdrawn) The aptamer of claim 42, wherein the target is a cell membrane receptor or a viral surface molecule.

45. (Withdrawn) A composition comprising the aptamer and the target of claim 42.

46. (Currently amended) A method of identifying an aptamer that binds to a target, ~~the target being capable of binding a target partner,~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for ~~the~~ a target partner comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a target partner~~/~~ or target partner analog or both under conditions that favor specific binding;

b) partitioning the bound nucleic acids from the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner[[/]] or target partner analog or both under conditions that disfavor efficient binding between the target and target partner[[/]] or target partner analog or both;

d) partitioning nucleic acids bound to a target-target partner complex or[[/]] a target-target partner analog complex from unbound nucleic acids; and

e) retaining the nucleic acids bound to ~~a target-target partner/analog~~ the complex, thereby identifying an aptamer that binds to a target ~~capable of~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for the ~~to a~~ target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

47. (Currently amended) A method of identifying an aptamer that binds to a target, ~~the target being capable of binding a target partner,~~ wherein the binding of the aptamer to the target

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increases the binding affinity of the target for ~~the~~ a target partner comprising the following steps:

a) contacting a target-based pool of nucleic acid molecules having high affinity and specificity for the target with the target and a target partner[[/]] or target partner analog or both under conditions that disfavor efficient binding between the target and a target partner[[/]] or target partner analog or both, wherein the target or target partner[[/]] or target partner analog is attached to a support;

b) partitioning nucleic acids bound to the support from unbound nucleic acids; and

c) retaining the nucleic acids associated with the support,

thereby identifying an aptamer that binds a target ~~capable of binding a target partner~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

48. (Previously presented) The method of claim 46, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

49. (Currently amended) The method of claim 46 or 48, wherein step e) further comprises removing the retained nucleic acids from the ~~target-target partner/analog~~ complex and amplifying the removed nucleic acids.

50. (Currently amended) The method of claim 47, wherein step c) further comprises removing the retained nucleic acids from the target-target partner complex [[/]] or target-target partner analog complex and amplifying the removed nucleic acids.

51. (Previously presented) The method of claim 49, further comprising repeating steps a) to e).

52. (Previously presented) The method of claim 50, further comprising repeating steps a) to c).

53. (Currently amended) The method of claim 51, wherein the target partner[[/]] or target partner analog or both are immobilized.

54. (Previously presented) The method of claim 51, wherein the target-based pool is

diversified.

55. (Previously presented) The method of claim 47, wherein the retaining step further comprises eluting the aptamer with an agonist competitor to the aptamer.

. 56. (Previously presented) The method of claim 49, wherein the retaining step further comprises eluting the aptamer with an agonist competitor to the aptamer.

57. (Previously presented) The method of claim 49, wherein the retaining step further comprises contacting the bound nucleic acids with excess free target.

58. (Withdrawn) An aptamer that specifically binds to the target, wherein the binding of the aptamer to the target regulates the binding of the target to the target partner and wherein the aptamer is obtainable by the method of claim 46.

59. (Withdrawn) The aptamer of claim 58, wherein the target is a cell surface receptor.

60. (Currently amended) A method of identifying an aptamer that binds to a target, the target being capable of binding an agonist competitor and a target partner, wherein the binding of the aptamer to the target increases the binding affinity of the target for the a target partner, comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a target partner[[/]] or target partner analog or both under conditions that favor specific binding;

b) partitioning the bound nucleic acids from the unbound nucleic acids;

c) binding the target to a target partner[[/]] or target partner analog or both to form a target-target partner/analog complex and contacting the target-target partner/ analog complex with the unbound nucleic acids under conditions that favor specific binding; and

d) removing nucleic acids with low binding affinity for the target-target partner/analog complex; and

e) combining an agonist competitor with the nucleic acids bound to the target-target partner/analog complex, eluting the nucleic acids, and amplifying the eluted nucleic acids,

thereby identifying an aptamer that binds a target capable of binding an agonist competitor and a target partner wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

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61. (Previously presented) The method of claim 60, further comprising repeating steps a) to e).

62. (Previously presented) The method of claim 61, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

63. (Previously presented) The method of claim 62, wherein the target-based pool is diversified.

64 (Currently amended) The method of claim 62, wherein the ~~target-target-partner/analog~~ complex is immobilized.

65. (Withdrawn) An aptamer that specifically binds to the target, wherein the binding of the aptamer to the target regulates the binding of the target to the target partner and wherein the aptamer is obtainable by the method of claim 60.

66. (Currently amended) A method of identifying an aptamer that binds to a target, ~~the target being capable of binding agonist competitor and a target partner,~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for ~~the~~ a target partner comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a complex of the target and agonist competitor under conditions that favor specific binding;

b) partitioning the bound nucleic acids from the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target under conditions that favor specific binding, wherein the target is immobilized;

d) partitioning the unbound nucleic acids from the bound nucleic acids; and

e) removing and retaining the bound nucleic acids from the immobilized target,

thereby identifying an aptamer that binds a target ~~capable of binding an agonist competitor and a target partner~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

67. (Currently amended) The method of claim 66, wherein complex of step a) further comprises the target partner[[/]] or target partner analog or both.

68. (Currently amended) The method of claim 66, wherein the immobilized target of step c) further comprises the target partner[[/]] or target partner analog or both.

69. (Currently amended) A method of identifying an aptamer that binds to a target, ~~the target being capable of binding an agonist competitor and a target partner,~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for ~~the~~ a target partner, comprising the following steps:

a) binding the target to the target partner[[/]] or target partner analog or both to form a ~~target-target partner/analog~~ complex and contacting the ~~target-target partner/analog~~ complex with a target-based pool of nucleic acid molecules having high affinity and specificity for the target under conditions that favor specific binding; and

b) removing nucleic acids with low binding affinity for the ~~target-target partner/analog~~ complex; and

c) retaining nucleic acids bound to the ~~target-target partner/analog~~ complex; and

d) combining an agonist competitor with the nucleic acids bound to ~~the target-target partner/analog~~ complex, eluting the nucleic acids, and amplifying the eluted nucleic acids,

thereby identifying an aptamer that binds a ~~target-capable of binding an agonist competitor and a target partner~~ wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

70. (Currently amended) The method of claim 69, further comprising the step of contacting a modified target, wherein the target is lacking regions required for target binding, with a target-based pool of nucleic acid molecules having high affinity and specificity for the target under conditions that favor specific binding; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the ~~target-target partner/analog~~ complex in step a).